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RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/866,557A

TIME: 15:45:41

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3 <110> APPLICANT: Hammond, S.
4     Hannon, G.
5     Beach, D.
7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
9 <130> FILE REFERENCE: GNCA-P02-007
11 <140> CURRENT APPLICATION NUMBER: 09/866,557A
C--> 12 <141> CURRENT FILING DATE: 2002-03-26
14 <150> PRIOR APPLICATION NUMBER: 60/189,739
15 <151> PRIOR FILING DATE: 2000-03-16
17 <150> PRIOR APPLICATION NUMBER: 60/243,097
18 <151> PRIOR FILING DATE: 2000-10-24
20 <160> NUMBER OF SEQ ID NOS: 5
22 <170> SOFTWARE: PatentIn version 3.1
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25 <211> LENGTH: 5775
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
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38 atg acc cct gct tcc tca cca atg ggt cct ttc ttt gga ctg cca tgg      96
39 Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp
40          20          25          30
41 caa caa gaa gca att cat gat aac att tat acg cca aga aaa tat cag      144
42 Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln
43          35          40          45
44 gtt gaa ctg ctt gaa gca gct ctg gat cat aat acc atc gtc tgt tta      192
45 Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu
46          50          55          60
47 aac act ggc tca ggg aag aca ttt att gct agt act act cta cta aag      240
48 Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys
49 65          70          75          80
50 agc tgt ctc tat cta gat cta ggg gag act tca gct aga aat gga aaa      288
51 Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys
52          85          90          95
53 agg acg gtg ttc ttg gtc aac tct gca aac cag gtt gct caa caa gtg      336
54 Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val
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57 Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn
58      115      120      125
59 cta gaa gta aat gca tct tgg aca aaa gag aga tgg aac caa gag ttt      432
60 Leu Glu Val Asn Ala Ser Trp Thr Lys Glu Arg Trp Asn Gln Glu Phe
61      130      135      140
62 act aag cac cag gtt ctc att atg act tgc tat gtc gcc ttg aat gtt      480
63 Thr Lys His Gln Val Leu Ile Met Thr Cys Tyr Val Ala Leu Asn Val
64 145      150      155      160
65 ttg aaa aat ggt tac tta tca ctg tca gac att aac ctt ttg gtg ttt      528
66 Leu Lys Asn Gly Tyr Leu Ser Leu Ser Asp Ile Asn Leu Leu Val Phe
67      165      170      175
68 gat gag tgt cat ctt gca atc cta gac cac ccc tat cga gaa ttt atg      576
69 Asp Glu Cys His Leu Ala Ile Leu Asp His Pro Tyr Arg Glu Phe Met
70      180      185      190
71 aag ctc tgt gaa att tgt cca tca tgt cct cgc att ttg gga cta act      624
72 Lys Leu Cys Glu Ile Cys Pro Ser Cys Pro Arg Ile Leu Gly Leu Thr
73      195      200      205
74 gct tcc att tta aat ggg aaa tgg gat cca gag gat ttg gaa gaa aag      672
75 Ala Ser Ile Leu Asn Gly Lys Trp Asp Pro Glu Asp Leu Glu Glu Lys
76      210      215      220
77 ttt cag aaa cta gag aaa att ctt aag agt aat gct gaa act gca act      720
78 Phe Gln Lys Leu Glu Lys Ile Leu Lys Ser Asn Ala Glu Thr Ala Thr
79 225      230      235      240
80 gac ctg gtg gtc tta gac agg tat act tct cag cca tgt gag att gtg      768
81 Asp Leu Val Val Leu Asp Arg Tyr Thr Ser Gln Pro Cys Glu Ile Val
82      245      250      255
83 gtg gat tgt gga cca ttt act gac aga agt ggg ctt tat gaa aga ctg      816
84 Val Asp Cys Gly Pro Phe Thr Asp Arg Ser Gly Leu Tyr Glu Arg Leu
85      260      265      270
86 ctg atg gaa tta gaa gaa gca ctt aat ttt atc aat gat tgt aat ata      864
87 Leu Met Glu Leu Glu Glu Ala Leu Asn Phe Ile Asn Asp Cys Asn Ile
88      275      280      285
89 tct gta cat tca aaa gaa aga gat tct act tta att tcg aaa cag ata      912
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92 cta tca gac tgt cgt gcc gta ttg gta gtt ctg gga ccc tgg tgt gca      960
93 Leu Ser Asp Cys Arg Ala Val Leu Val Val Leu Gly Pro Trp Cys Ala
94 305      310      315      320
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96 Asp Lys Val Ala Gly Met Met Val Arg Glu Leu Gln Lys Tyr Ile Lys
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98 cat gag caa gag gag ctg cac agg aaa ttt tta ttg ttt aca gac act      1056
99 His Glu Gln Glu Glu Leu His Arg Lys Phe Leu Leu Phe Thr Asp Thr
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101 ttc cta agg aaa ata cat gca cta tgt gaa gag cac ttc tca cct gcc      1104
102 Phe Leu Arg Lys Ile His Ala Leu Cys Glu Glu His Phe Ser Pro Ala
103      355      360      365
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108 Ile Leu Arg Lys Tyr Lys Pro Tyr Glu Arg His Ser Phe Glu Ser Val
109 385                      390                      395                      400
110 gag tgg tat aat aat aga aat cag gat aat tat gtg tca tgg agt gat      1248
111 Glu Trp Tyr Asn Asn Arg Asn Gln Asp Asn Tyr Val Ser Trp Ser Asp
112                      405                      410                      415
113 tct gag gat gat gat gag gat gaa gaa att gaa gaa aaa gag aag cca      1296
114 Ser Glu Asp Asp Asp Glu Asp Glu Glu Ile Glu Glu Lys Glu Lys Pro
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116 gag aca aat ttt cct tct cct ttt acc aac att ttg tgc gga att att      1344
117 Glu Thr Asn Phe Pro Ser Pro Phe Thr Asn Ile Leu Cys Gly Ile Ile
118                      435                      440                      445
119 ttt gtg gaa aga aga tac aca gca gtt gtc tta aac aga ttg ata aag      1392
120 Phe Val Glu Arg Arg Tyr Thr Ala Val Val Leu Asn Arg Leu Ile Lys
121      450                      455                      460
122 gaa gct ggc aaa caa gat cca gag ctg gct tat atc agt agc aat ttc      1440
123 Glu Ala Gly Lys Gln Asp Pro Glu Leu Ala Tyr Ile Ser Ser Asn Phe
124 465                      470                      475                      480
125 ata act gga cat ggc att ggg aag aat cag cct cgc aac aac acg atg      1488
126 Ile Thr Gly His Gly Ile Gly Lys Asn Gln Pro Arg Asn Asn Thr Met
127                      485                      490                      495
128 gaa gca gaa ttc aga aaa cag gaa gag gta ctt agg aaa ttt cga gca      1536
129 Glu Ala Glu Phe Arg Lys Gln Glu Glu Val Leu Arg Lys Phe Arg Ala
130                      500                      505                      510
131 cat gag acc aac ctg ctt att gca aca agt att gta gaa gag ggt gtt      1584
132 His Glu Thr Asn Leu Leu Ile Ala Thr Ser Ile Val Glu Glu Gly Val
133                      515                      520                      525
134 gat ata cca aaa tgc aac ttg gtg gtt cgt ttt gat ttg ccc aca gaa      1632
135 Asp Ile Pro Lys Cys Asn Leu Val Val Arg Phe Asp Leu Pro Thr Glu
136      530                      535                      540
137 tat cga tcc tat gtt caa tct aaa gga aga gca agg gca ccc atc tct      1680
138 Tyr Arg Ser Tyr Val Gln Ser Lys Gly Arg Ala Arg Ala Pro Ile Ser
139 545                      550                      555                      560
140 aat tat ata atg tta gcg gat aca gac aaa ata aaa agt ttt gaa gaa      1728
141 Asn Tyr Ile Met Leu Ala Asp Thr Asp Lys Ile Lys Ser Phe Glu Glu
142                      565                      570                      575
143 gac ctt aaa acc tac aaa gct att gaa aag atc ttg aga aac aag tgt      1776
144 Asp Leu Lys Thr Tyr Lys Ala Ile Glu Lys Ile Leu Arg Asn Lys Cys
145                      580                      585                      590
146 tcc aag tcg gtt gat act ggt gag act gac att gat cct gtc atg gat      1824
147 Ser Lys Ser Val Asp Thr Gly Glu Thr Asp Ile Asp Pro Val Met Asp
148                      595                      600                      605
149 gat gat cac gtt ttc cca cca tat gtg ttg agg cct gac gat ggt ggt      1872
150 Asp Asp His Val Phe Pro Pro Tyr Val Leu Arg Pro Asp Asp Gly Gly
151      610                      615                      620
152 cca cga gtc aca atc aac acg gcc att gga cac atc aat aga tac tgt      1920
153 Pro Arg Val Thr Ile Asn Thr Ala Ile Gly His Ile Asn Arg Tyr Cys

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156	Ala	Arg	Leu	Pro	Ser	Asp	Pro	Phe	Thr	His	Leu	Ala	Pro	Lys	Cys	Arg	
157					645							650			655		
158	acc	cga	gag	ttg	cct	gat	ggt	aca	ttt	tat	tca	act	ctt	tat	ctg	cca	2016
159	Thr	Arg	Glu	Leu	Pro	Asp	Gly	Thr	Phe	Tyr	Ser	Thr	Leu	Tyr	Leu	Pro	
160				660					665					670			
161	att	aac	tca	cct	ctt	cga	gcc	tcc	att	gtt	ggt	cca	cca	atg	agc	tgt	2064
162	Ile	Asn	Ser	Pro	Leu	Arg	Ala	Ser	Ile	Val	Gly	Pro	Pro	Met	Ser	Cys	
163			675					680						685			
164	gta	cga	ttg	gct	gaa	aga	gtt	gtc	gct	ctc	att	tgc	tgt	gag	aaa	ctg	2112
165	Val	Arg	Leu	Ala	Glu	Arg	Val	Val	Ala	Leu	Ile	Cys	Cys	Glu	Lys	Leu	
166			690					695						700			
167	cac	aaa	att	ggc	gaa	ctg	gat	gac	cat	ttg	atg	cca	gtt	ggg	aaa	gag	2160
168	His	Lys	Ile	Gly	Glu	Leu	Asp	Asp	His	Leu	Met	Pro	Val	Gly	Lys	Glu	
169	705					710						715				720	
170	act	gtt	aaa	tat	gaa	gag	gag	ctt	gat	ttg	cat	gat	gaa	gaa	gag	acc	2208
171	Thr	Val	Lys	Tyr	Glu	Glu	Glu	Leu	Asp	Leu	His	Asp	Glu	Glu	Glu	Thr	
172				725							730				735		
173	agt	gtt	cca	gga	aga	cca	ggt	tcc	acg	aaa	cga	agg	cag	tgc	tac	cca	2256
174	Ser	Val	Pro	Gly	Arg	Pro	Gly	Ser	Thr	Lys	Arg	Arg	Gln	Cys	Tyr	Pro	
175				740							745				750		
176	aaa	gca	att	cca	gag	tgt	ttg	agg	gat	agt	tat	ccc	aga	cct	gat	cag	2304
177	Lys	Ala	Ile	Pro	Glu	Cys	Leu	Arg	Asp	Ser	Tyr	Pro	Arg	Pro	Asp	Gln	
178			755					760						765			
179	ccc	tgt	tac	ctg	tat	gtg	ata	gga	atg	gtt	tta	act	aca	cct	tta	cct	2352
180	Pro	Cys	Tyr	Leu	Tyr	Val	Ile	Gly	Met	Val	Leu	Thr	Thr	Pro	Leu	Pro	
181			770					775						780			
182	gat	gaa	ctc	aac	ttt	aga	agg	cgg	aag	ctc	tat	cct	cct	gaa	gat	acc	2400
183	Asp	Glu	Leu	Asn	Phe	Arg	Arg	Arg	Lys	Leu	Tyr	Pro	Pro	Glu	Asp	Thr	
184	785					790								795		800	
185	aca	aga	tgc	ttt	gga	ata	ctg	acg	gcc	aaa	ccc	ata	cct	cag	att	cca	2448
186	Thr	Arg	Cys	Phe	Gly	Ile	Leu	Thr	Ala	Lys	Pro	Ile	Pro	Gln	Ile	Pro	
187				805							810				815		
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189	His	Phe	Pro	Val	Tyr	Thr	Arg	Ser	Gly	Glu	Val	Thr	Ile	Ser	Ile	Glu	
190				820							825				830		
191	ttg	aag	aag	tct	ggt	ttc	atg	ttg	tct	cta	caa	atg	ctt	gag	ttg	att	2544
192	Leu	Lys	Lys	Ser	Gly	Phe	Met	Leu	Ser	Leu	Gln	Met	Leu	Glu	Leu	Ile	
193			835							840				845			
194	aca	aga	ctt	cac	cag	tat	ata	ttc	tca	cat	att	ctt	cgg	ctt	gaa	aaa	2592
195	Thr	Arg	Leu	His	Gln	Tyr	Ile	Phe	Ser	His	Ile	Leu	Arg	Leu	Glu	Lys	
196			850					855						860			
197	cct	gca	cta	gaa	ttt	aaa	cct	aca	gac	gct	gat	tca	gca	tac	tgt	gtt	2640
198	Pro	Ala	Leu	Glu	Phe	Lys	Pro	Thr	Asp	Ala	Asp	Ser	Ala	Tyr	Cys	Val	
199	865					870								875		880	
200	cta	cct	ctt	aat	gtt	gtt	aat	gac	tcc	agc	act	ttg	gat	att	gac	ttt	2688
201	Leu	Pro	Leu	Asn	Val	Val	Asn	Asp	Ser	Ser	Thr	Leu	Asp	Ile	Asp	Phe	
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206	agt	aca	aag	tat	aca	aaa	gaa	aca	ccc	ttt	ggt	ttt	aaa	tta	gaa	gat	2784
207	Ser	Thr	Lys	Tyr	Thr	Lys	Glu	Thr	Pro	Phe	Val	Phe	Lys	Leu	Glu	Asp	
208			915					920						925			
209	tac	caa	gat	gcc	ggt	atc	att	cca	aga	tat	cgc	aat	ttt	gat	cag	cct	2832
210	Tyr	Gln	Asp	Ala	Val	Ile	Ile	Pro	Arg	Tyr	Arg	Asn	Phe	Asp	Gln	Pro	
211		930					935						940				
212	cat	cga	ttt	tat	gta	gct	gat	gtg	tac	act	gat	ctt	acc	cca	ctc	agt	2880
213	His	Arg	Phe	Tyr	Val	Ala	Asp	Val	Tyr	Thr	Asp	Leu	Thr	Pro	Leu	Ser	
214	945				950					955					960		
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216	Lys	Phe	Pro	Ser	Pro	Glu	Tyr	Glu	Thr	Phe	Ala	Glu	Tyr	Tyr	Lys	Thr	
217				965						970					975		
218	aag	tac	aac	ctt	gac	cta	acc	aat	ctc	aac	cag	cca	ctg	ctg	gat	gtg	2976
219	Lys	Tyr	Asn	Leu	Asp	Leu	Thr	Asn	Leu	Asn	Gln	Pro	Leu	Leu	Asp	Val	
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221	gac	cac	aca	tct	tca	aga	ctt	aat	ctt	ttg	aca	cct	cga	cat	ttg	aat	3024
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228	Ala	Lys	Trp	Glu	Ser	Leu	Gln	Asn	Lys	Gln	Ile	Leu	Val	Pro	Glu		
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238		1070					1075						1080				
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241		1085					1090						1095				
242	ggg	tgg	aaa	aaa	tct	att	gac	agc	aaa	tct	ttc	atc	tca	att	tct		3339
243	Gly	Trp	Lys	Lys	Ser	Ile	Asp	Ser	Lys	Ser	Phe	Ile	Ser	Ile	Ser		
244		1100					1105						1110				
245	aac	tcc	tct	tca	gct	gaa	aat	gat	aat	tac	tgt	aag	cac	agc	aca		3384
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